```
                  5'UTR                          M   D   L   V   L   R   K   Y   L   L      10
-29 GGTCTTTGGTTGCTGGAAGGAAGAACAGG  -1 +1 ATG GAT CTG GTG CTG AGA AAA TAC CTT CTC       30
SIL5 ─────────────────────────────►

      H   V   A   L   M   G   V   L   L   A   V   R   T   T   E   G   P   R            28
     CAT GTG GCT CTG ATG GGT GTT CTT CTG GCT GTA AGG ACC ACA GAA GGA CCC AGA          84

      D   R   D   W   L   G   V   S   R   Q   L   R   I   K   A   W   N   R            46
     GAC AGG GAC TGG CTT GGT GTC TCA AGG CAG CTC AGA ATT AAA GCA TGG AAC AGA         138

      Q   L   Y   P   E   W   T   E   S   Q   G   P   D   C   W   R   G   G            64
     CAG CTG TAT CCA GAG TGG ACA GAA AGC CAG GGG CCT GAC TGC TGG AGA GGT GGC         192

      H   I   S   L   K   V   S   N   D   G   P   T   L   I   G   A   N   A            82
     CAC ATA TCC CTG AAG GTC AGC AAT GAT GGG CCT ACA CTG ATT GGG GCA AAT GCT         246

      S   F   S   I   A   L   H   F   P   K   S   Q   K   V   L   P   D   G           100
     TCC TTC TCT ATT GCC TTG CAC TTT CCT AAA AGC CAA AAG GTG CTG CCA GAT GGG ◄── SIL2 300

      Q   V   I   W   A   N   N   T   I   I   N   G   S   Q   V   W   G   G           118
     CAG GTC ATC TGG GCC AAC AAC ACC ATC ATC AAT GGG AGC CAG GTG TGG GGA GGA ◄── SIL1 354

      Q   L   V   Y   P   Q   E   P   D   D   T   C   I   F   P   D   G   E           136
     CAG CTG GTA TAT CCC CAA GAA CCT GAT GAT ACC TGC ATC TTC CCC GAT GGG GAG         408

      P   C   P   S   G   P   L   S   Q   K   R   C   F   V   Y   V   W   K           154
     CCC TGC CCT TCT GGC CCT CTA TCT CAG AAA AGA TGC TTT GTT TAT GTC TGG AAG         462

      T   W   D   Q   Y   W   Q   V   L   G   G   P   V   S   G   L   S   I           172
     ACC TGG GAC CAA TAC TGG CAA GTT CTG GGG GGC CCA GTG TCT GGA CTG AGC ATC         516

      G   T   D   K   A   M   L   G   T   Y   N   M   E   V   T   V   Y   H           190
     GGG ACA GAC AAG GCA ATG CTG GGC ACA TAT AAC ATG GAA GTG ACT GTC TAC CAC         570

      R   R   G   S   Q   S   Y   V   P   L   A   H   S   S   S   A   F   T           208
     CGC CGG GGG TCC CAG AGC TAT GTG CCC CTC GCT CAC TCC AGT TCA GCC TTC ACC         624

      I   T   D   Q   V   P   F   S   V   S   V   S   Q   L   Q   A   L   D           226
     ATT ACT GAC CAG GTG CCC TTC TCT GTG AGT GTG TCT CAG CTG CAG GCC TTG GAT         678

      G   R   N   K   R   F   L   R   K   Q   P   L   T   F   A   L   Q   L           244
     GGA AGG AAC AAG CGC TTC CTG AGA AAG CAG CCT CTG ACC TTT GCC CTC CAG CTC         732

      H   D   P   S   G   Y   L   A   G   A   D   L   S   Y   T   W   D   F           262
     CAT GAT CCC AGT GGC TAT TTG GCT GGG GCT GAC CTT TCC TAC ACC TGG GAC TTT         786

      G   D   S   T   G   T   L   I   S   R   A   L   T   V   T   H   T   Y           280
     GGT GAC AGT ACA GGG ACC CTG ATC TCT CGG GCA CTC ACG GTC ACT CAC ACT TAC         840

      L   E   S   G   P   V   T   A   Q   V   V   L   Q   A   A   I   P   L           298
     CTA GAG TCT GGC CCA GTC ACT GCA CAG GTG GTG CTG CAG GCT GCC ATT CCT CTC         894

      T   S   C   G   S   S   P   V   P   G   T   T   D   R   H   V   T   T           316
     ACC TCC TGT GGC TCC TCT CCA GTT CCA GGC ACT ACA GAT AGG CAT GTG ACA ACT         948

      A   E   A   P   G   T   T   A   G   Q   V   P   T   T   E   V   M   G           334
     GCA GAG GCT CCT GGA ACC ACA GCT GGC CAA GTG CCT ACT ACA GAA GTC ATG GGC        1002

      T   T   P   G   Q   V   P   T   A   E   A   P   G   T   T   V   G   W           352
     ACC ACA CCT GGC CAG GTG CCA ACT GCA GAG GCC CCT GGC ACC ACA GTT GGG TGG        1056

      V   P   T   T   E   D   V   G   T   T   P   E   Q   V   A   T   S   K           370
     GTG CCA ACC ACA GAG GAT GTA GGT ACC ACA CCT GAG CAG GTG GCA ACC TCC AAA        1110

      V   L   S   T   T   P   V   E   M   P   T   A   K   A   T   G   R   T           388
     GTC TTA AGT ACA ACA CCA GTG GAG ATG CCA ACT GCA AAA GCT ACA GGT AGG ACA        1164
```

Figure 1

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P     E     V     S     T     T     E     P     S     G     T     T     V     T     Q     G     T     T        406
CCT   GAA   GTG   TCA   ACT   ACA   GAG   CCC   TCT   GGA   ACC   ACA   GTT   ACA   CAG   GGA   ACA   ACT      1218

P     E     L     V     E     T     T     A     G     E     V     S     T     P     E     P     A     G        424
CCA   GAG   CTG   GTG   GAG   ACC   ACA   GCT   GGA   GAG   GTG   TCC   ACT   CCT   GAG   CCT   GCG   GGT      1272

S     N     T     S     S     F     M     P     T     E     G     T     A     G     S     L     S     P        442
TCA   AAT   ACT   AGC   TCA   TTC   ATG   CCT   ACA   GAA   GGT   ACT   GCA   GGC   TCC   CTG   AGT   CCC      1326

L     P     D     D     T     A     T     L     V     L     E     K     R     Q     A     P     L     D        460
CTG   CCG   GAT   GAC   ACT   GCC   ACC   TTA   GTC   CTG   GAG   AAG   CGC   CAA   GCC   CCC   CTG   GAT      1380

C     V     L     Y     R     Y     G     S     F     S     L     T     L     D     I     V     Q     G        478
TGT   GTT   CTG   TAT   CGC   TAT   GGC   TCC   TTT   TCC   CTC   ACC   CTG   GAC   ATT   GTC   CAG   GGT      1434

I     E     S     A     E     I     L     Q     A     V     S     S     S     E     G     D     A     F        496
ATT   GAG   AGT   GCT   GAG   ATC   CTA   CAG   GCT   GTG   TCA   TCC   AGT   GAA   GGA   GAT   GCA   TTT      1488

E     L     T     V     S     C     Q     G     G     L     P     K     E     A     C     M     D     I        514
GAG   CTG   ACT   GTG   TCT   TGC   CAA   GGC   GGG   CTA   CCC   AAG   GAA   GCC   TGC   ATG   GAC   ATC      1542

S     S     P     G     C     Q     L     P     A     Q     R     L     C     Q     P     V     P     P        532
TCA   TCG   CCA   GGG   TGT   CAG   CTG   CCT   GCC   CAG   CGG   CTG   TGT   CAG   CCT   GTG   CCC   CCC      1596

S     P     A     C     Q     L     V     L     H     Q     V     L     K     G     G     S     G     T        550
AGC   CCA   GCC   TGC   CAG   CTG   GTT   TTG   CAC   CAG   GTA   CTG   AAG   GGT   GGC   TCA   GGG   ACC      1650

Y     C     L     N     V     S     L     A     D     A     N     S     L     A     M     V     S     T        568
TAC   TGC   CTC   AAT   GTG   TCT   TTG   GCT   GAT   GCC   AAT   AGC   CTG   GCG   ATG   GTC   AGC   ACC      1704
SIL3──────────────────────────────────────────────▶

Q     L     V     M     P     G     Q     E     A     G     L     R     Q     A     P     L     F     V        586
CAG   CTT   GTC   ATG   CCT   GGG   CAA   GAA   GCA   GGC   CTC   AGG   CAG   GCT   CCT   CTG   TTC   GTG      1758

G     I     L     L     V     L     T     A     L     L     L     A     S     L     I     Y     R     R        604
GGC   ATC   TTG   CTG   GTG   CTA   ACA   GCT   TTG   TTG   CTT   GCA   TCT   CTG   ATA   TAC   AGG   CGA      1812

R     L     M     K     Q     G     S     A     V     P     L     P     Q     L     P     H     G     R        622
AGA   CTT   ATG   AAG   CAA   GGC   TCA   GCA   GTC   CCC   CTT   CCC   CAG   CTG   CCA   CAC   GGT   AGA      1866

T     Q     W     L     R     L     P     W     V     F     R     S     C     P     I     G     E     S        640
ACC   CAG   TGG   CTA   CGT   CTG   CCC   TGG   GTC   TTC   CGC   TCT   TGC   CCC   ATT   GGT   GAG   AGC      1920

K     P     L     L     S     G     Q     Q     V     *     ◀──────────────────────────────SIL7  649
AAA   CCC   CTC   CTC   AGT   GGA   CAG   CAG   GTC   TGA   GTG   CTC   TTA   TGT   GAA   GTC   ATG   ATT      1974
SIL4──────────────────────────────────────────────▶

TAC   CCA   GGT   GGA   CAG   CAA   GGC   CTG   TCT   TTT   CTC   TGG   TCT   TCC   CTC   AGA   GAC   TAC      2028
      ◀──────────────────────────────────────SIL6              (SEQ ID NO: 13)

CAT   TGC   CTG   AAA   TAA   AGA   CTC   AGA   ACT   TG          Poly(A)      (SEQ ID NO: 12)                 2057
◀─────────────────────────────────────SIL9
               3'UTR
```

Figure 1 (suite)

SIL10
GTTGCTGGAAGGAAGAACAGG**ATGGATCTGGTGCTGAGAAAA**TACCTTCTCCATGTGGCTCTGATGGGTGTTCTTCTGGC 80

TGTAAGGACCACAGAAGGTGAGTGTGGGATGTTGGACATGAACAAGTGTGAATTTGGGGTTGCACACCTGCTCTGGTTTT 160

TCTCTCCCTAAAATGGAAGATATCAGTAGTGCTTCAGGTGTCTCCCACCCATTTGATTTAGTGAGGACATGGGCAACTGA 240

GCTCCCTCCCCACATGAAGATTTGGGTGCATGTGTGTTCAGGCACTTGGGACTGAACCTGAAAACAACCCCATCTACCTG 320
                                    ◄――――――――――――――――――――――――――**SIL8**
GATGGGTGAGAGAACAGTATGTCTCCGTGGCCCTAATTTTGAGATGCTCTGAATAGTGAGCTGGAACATGGGTGCCAAGG 400

TAGTAAAATGAGTGGAAACTCATTTAGGCTTTGTCTCAGGCACTTGGGATAGGGTATTTAGGAGATAGAGAAAGATAGGA 480

GATAGGAGAAAGGAGAAAGAGGATGTGGTATTGGATAGAAGGGTAATGAGGCACCTCATCCCCTCTTTGGGATGGGCATG 560

GGTGAACACAGCCCAGGCTTTTGTTCTGGGGCTGGAAGAGACAGGCAGAAGGGTCTCAGCTGAGCATCACATGAAAGGGC 640

TCTGGGGGATTGGGGCCTCGTGACAGGAGCAAGGCGGGTGGGGTGGGGATGGTGAGAGGGTCTGGAATGTCCCGTGCTGC 720

TCTGAGGAGGGAGGATTGGGAGTGGAGAAAGAATGGGGCATCTTATGATTCTCTTGTTCTTGTGGTGAGGTATTCAGTGG 800

GATAATTCTAGATCCTCCCCCAAGAGAATCAACCAGGTTTCTGGTACATGTTAGAGATGGAGTGAGGATAGTCTGTGATG 880

TGCAGAAATATCTACATTGTACCCCAGTGCCCCCTTTCTCTAGATCCCTGGTCTCACAGACTTCTTGGAACTTCTCCTTG 960

ATCTGACTTCCCTCATTCATGGTGTCATTTCAAGTCTTATTCTTTTACTATGTTCGTTATTGTATTCTGGAAATATCCTG 1040

TTCATATGTGTCCACCCAAGGCTCTTAATATGTTGTGCTTACTTTTTGGATCCAGATTTTTAAAATCATAAGAAGACATT 1120

TTTATATAGTTCATGAAATTTTGCATGGACTGAGTTTGATAATTTTGTTTAGTGTGAATTAACATTGTGTTTATTTAAGA 1200

AAAAAAAATATTTTTTTACAGAAACCTACTGAATTTGTAGGGTTTTAAAATAACATGATGTCTGGGATTTGCTTTTGAAT 1280

GCTTCAGCCAAAAAACAAACGAACAACAAAAATAAAGGATAGATAAAGCAAATGTGACAAAATGCTGATAGTTGTTGGAC 1360

CTTGGGGAGACACATGCAGAGCCATCACATCACTTTTTTTCAGACATCTTTCTTGGTCAGTTATAATCATTTTGTTTGTC 1440

CCCACTCCCAATTTCTACTTGCCTCTAGTCCATCCTCCTCACTGCTTGCCAAAGTGATCCTTCTAAAACACAAATCTGAT 1520

CATATTCAAAAAGCTTTTGAAGGGTAAGTTTTATGGTATATGCCATATATCAGTACAACAAACAAAATCGTCTGAGGTGC 1600

CGTTGCCTACAGGATAAAGTCCAAACTCCTTTGCCTGGCACTCCAAGCCCCCACTCTATCTTCTTGGCCTCATCTCTCAT 1680

GATGTACATCAGCCACATTGCTAGTGTCTGCTCATGGCCTTCTGCCTAGAATGCTTTATGCCCCAGCCAACTATTTACTG 1760

TCTTCTTCAGTCGACCAGAGTGCAATTTACCTGTTTAAAATCTATCATTTTGTTATACATTGTGCATGTCTATTATGGCT 1840

CATATTAAGCAATGCCTTGGATTATAGTAATTTATGTATATGTCTATTTCATATACTTTAACCTGAACCCCTTCAGAACC 1920

ATTTCTTTTTCATTTCTTAAGTTCTTTGCACCTAGCCCAGTGCCTGGTACGTCGTGGGTATTCAGTAGATTAAAATGCAC 2000

TTTAAGGAACTTCCCTTGTTGTCCATCAAGTGGCTAAGGCTCTGTGCTCCCAATGCAGGGGACCAGGGTTCAATCTCAGG 2080

TCAGGGAACTAGATCCCACAGGTCACAACTAAGAGTTTGCAAGCCACAACTACCTGACCTCACATGCCACAACTAATCGA 2160

AGATCCCTCGTGCTGCAACTAAGTCCTAGTGCAGTTAAATATATTTTTTTAATGCACTTTGAATGTGAGAATGAATGATG 2240

TGTCACAGACACTGTTGTCCCCTGAGAAGGGAGTGAGTAATGATTTGAGGGCCCTCATAGTATATCTTCCTTTTT**AGGAC** 2320

CCAGAGACAGGGACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAGAGTGGACA 2400

GAAAGCCAGGGGCCTGACTGCTGGAGAGGTAGGAACTTGGCAATTTCCAGGGAGGATATGGTGGAAATGGGTGGGGAGGG 2480

GAACGGGGTTGAATGTACTTAGGAAGATAGGGAAGGAAAAGGCATACAGGGAGGAGAAGCCAAGGAGCTAATTAATGCAG 2560

CTGCCCTTTTCAGGTGGCCACATATCCCTGAAGGTCAGCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTC 2640

TATTGCCTTGCACTTTCCTAAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCAATG 2720

GTGAGTACCTCTCCGCCTCCTTCCCAAGGTCCAGAATCCCTGGTATCCCCAATGAGCTCAAGGAATCCTCCTCCTCTTTT 2800

TTTTTTTTTTTTTTTACAAATTATATATGTAACACATATTCACTGCAGAAAAATTAGAAAACACAGATAAACCAAAAGA 2880

Figure 2

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AAAAAAATTATAGTTCCCCAAATGGGGCACAGAAGACCCAGTGGACATAGAAGTTGGATAGACTTGGATTTAAACTGGTT    2960

ACCAGTATGTGACCCTGGACAAGTCACTGAATTGTTTTGTTCTTCCATTCCCTTATCTATAGAATGGGGATGATAACACT    3040

TTAAAAGGTTCTTGTAAGGATTAAAATGTGATAATATATAAAGATTTTAGCATAATGCCTGCCCTGTGCTGTGCTTAGTA    3120

CCTTAGTTTAGACGCTTTGCAACCCCATGGACTGTAGCCCACCAGGCTCCTCTGTCCATGTGGATTCTGCAGGCAAGAAT    3200

ACTGGAGTGGGTCACCATGCACTCCTCAGGGGATCTTCCCAACTCAGGGATCGAACCCAGGTCCTAGCCTACAGTATTA    3280

ATTGATGCTGTTATTTTTACTTTTATCCCACTAGCTAGAGCACATCATCCTAGACATTTTGATACATGGCCTACCAATTT    3360

GTGTCCAGTGTAAGAATATACATGTGTGTGCTCAGTGGCTCAGTCGTGTCTGACTCTTTGCAACCCCATGGACTGTAGCC    3440

CGCGAAAGCTCCTCTGCCCATGGGATTGCCCAGCCAAGAATACTGGAGCAGGTTGCCATTTCTTCCTCCAGGGGATCTTT    3520

CAACACAGGGATTGAATCCTTGTCTCCTGTGTTTCCTGCATTGGCAGGTGTATTCTTTACCACTGAGCCACCTGGGAAAC    3600

CCCTTAAGTATATACACATAAATCTTTTATAGTTTCCATTCTCCCTTCTACCACTCCAAATAGGTTATACCAAGGAGAAT    3680

GTATTTTGGTAGCTAGGCAGTATTCCTGGAGCCCCTCTCTGGGAGTCATGTTAAAGGTTTTGGTGTACAGTGAGGAATGC    3760

CAGGGATTGAGGGAGACTTGCTGTCTTCTTTTCAGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTG    3840

ATGATACCTGCATCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTTATGTCTGG    3920

AAGACCTGGGGTAAGAGTTTCCCTTCTCTGGCCTGTCATTCACACTTAAATTCACTTCTTCCTACCTGATCCCCTTTCTT    4000

TTGGTCTCATCCTTAAATTCTGTGAGTTTCCCTAATCTTCACTTCCCCCATGACTCCTTCCTCTTCCACAGCACCTAGTC    4080

AACTCTATTATACTTCTTTCTGGGAGCCCTGCTCCAATTATAGTCCCATCCCATGGACCCTCTCATAAGGACTTTTTTCC    4160

TGCCCAACATATGCAAGCTTAAACTCTCTGAAATAACCATCCTTGATACATCTCCTGACCTTCCTTCTCTGGTTCCATCT    4240

CTAACCCTGCCCCAGTCTCCTTTGACCAGTAACCCCCTTCCCTACTCTTCTTTCCAAAAACCTCAGACCAATACTGGCAA    4320

GTTCTGGGGGGCCCAGTGTCTGGACTGAGCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGT    4400

CTACCACCGCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTGGTAAGGACTGAG    4480

GAGGGGACAAGGCCAGTTGCAGGGCAGGAGAAGGTGGGGAGGCTGGGCTGGACAGGAAAGGGGAAAGAGGAAATGGTGTG    4560

TAACCTTACAGGGGCAGAACCAGGAAGATGTGGGCAGAGGGATGTGGGGCTTGGAGCCCGTGAAGGGCCAGGCAGCTTGG    4640

GTTGGTTGAAAAATATGGCTGTGAAAGAAGAAGCTGACAGAAAGAAGAACTTATGGTTCTCACTTTCTCTGACTCCAATC    4720

CCAGACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGCGCTTCCTGAGAAAGCA    4800

GCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATTTGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTG    4880

GTGACAGTACAGGGACCCTGATCTCTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAG    4960

GTGGTGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAGATAGGCATGTGACAAC    5040

TGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAGAAGTCATGGGCACCACACCTGGCCAGGTGCCAACTG    5120

CAGAGGCCCCTGGCACCACAGTTGGGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCC    5200

AAAGTCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAGTGTCAACTACAGAGCC    5280

CTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGGAGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTG    5360

CGGGTTCAAATACTAGCTCATTCATGCCTACAGAAGGTACTGCAGGTAAGGGGGCCACCATGAATGAGTTCATAGAGGTG    5440

GGGCATTTGTCACAGCTCTGAAGACCTGAAAGAATTGCTCAGGACCCAGATGTTACTCAATCCTTAGCTTAGCAGTGGAG    5520

TCCCCTCAGAATCTTCACTGGTTTTAAAACCCCCTAAGTCCCTCTTAATGGCACAGAATAGATCCAGAGTTCAGGAAACC    5600

AGGGTCTTCTCCTAGGCCAGGGGTAGAGAGCTTATTCTCTCTTCCTGAAGAGAAGTTCAGGAAGCAGTGTGTGATCATTT    5680

GGTGGTGGTGCTCAGTCATGTCTGACTCTTTGTGACCTCATGGACTATGGCCCACCAGGCTCCTCTGTCCATAGAATTCT    5760
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Figure 2 (suite 1)

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CCAGGCAAGAACACTGGAGTGGGTGGCCATTTCCTTCTCCAGGGGATTTTCCCTGCCCAGGGATTAAACCCGAATTGGCA    5840

GGTGGATTCTTTACCCGAGCCACCTAGAAAGTCCCATGTGATCATTAGATAATACTTATACCTCATTTTCTGATTAAGTG    5920

TAAACACAGAAATCTTTCTGACACCACTTCCCACCCCTGGATTCCCATCCCAAAGTAGGTTTACCTGGAATTGTGGTAGG    6000

AATACTAAAAAGGGAGAAGTGAGATAGTGACACTATGACTTAACACATGTCAAATGTCTGACCCAGGACCTGGCACAGTG    6080

TAGGGTGTGATAAACATTTGGGATGTCTAAAATTCTGACTCTAACCCTGTGACTCTGGGGCAGTCATTTCTCTTGGGCCT    6160

TTCTTTATCTTAAAAAATGAGAGTTTCCAGCTCTTGTCTGATTCTAAGCCTGGATCCAGTAGCTCTGACTCTACCTGGAA    6240

AAATGCTTGTTGGGCCTGTTTTCAGGTTAGTCATTTGCTTTTTGACTTTGCCTCTTTAATCCTCTCCTCCAGGCTCCCTG    6320

AGTCCCCTGCCGGATGACACTGCCACCTTAGTCCTGGAGAAGCGCCAAGCCCCCTGGATTGTGTTCTGTATCGCTATGG    6400

CTCCTTTTCCCTCACCCTGGACATTGTCCGTGAGTCTTGCCTACATTGTCCGTAAGCTGGTGGAGGGAGGCGTGTGCTGC    6480

TTAGGGTTGCCCAGTGGAAGCACACCTTGGAAGGAATTACTCACCTGGACAAGGAGAATACCCAGATCCCAGGGGTTTCA    6560

TATGAAGGCAGAATGGGATTAGGGAGGCAGCCCGAGGACCTTCCTGGCCATGGGCCTTGGGGGAGGATAAGTAGAGGAGT    6640

CTCAGACTTAAAAAAATCTTGCAACTTTGCAGAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCAGTGAAG    6720

GAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGTGAGTGTCCCACGGTTGCCCTGAGAACTCCTGGGGTGACTGC    6800

TGTCCTGTTCTCTGGTGTCTAGTGTCCCTTCCCAGATTCCCTGACGTAAGCTGACATCTCTCCCAGGCTACCCAAGGAAG    6880

CCTGCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGCCCCCCAGCCCAGCCTGC    6960

CAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCTACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCT    7040

GGCGATGGTCAGCACCCAGCTTGTCATGCCTGGTAGGTAGTTGGACAAGAGGTAGGATGAAGACACGGGGAGATGGTAGA    7120

GGTTACCTACTAGAGGAAGCAGACACTGAATGCAGCCGTATCTGGGATTCCACCCATAGGGCAAGAAGCAGGCCTCAGGC    7200

AGGCTCCTCTGTTCGTGGGCATCTTGCTGGTGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGTGAGATCCCCGC    7280

CATCCTGCTCCCACTCCTTTACCCCTTATTACCACCACCACTCTTCCTCATGGGAAGAAGAAACCACCAACCCCTTTGGG    7360

AAAGTGTAGAGTCCAAGAAAGAGCCCAGACTTGGAAGTTCAACAGGTCTAGGCTGCAGTCTTGCTGGTGGGACCCTGGGG    7440

AAGTCCATTAACCCTTCTGAGCCACTGAAAAGTAGGAAACATAATACCTGTCCTGTGGGGCTGTTTTCAGGGCTCTAGAC    7520

AATGTGAGTAAAACACCTGGTTCTGAAACAAAAGTGGAATAAATGATGATCTCAATGACTGTTGTTATGAATAATATCAA    7600

CAGTGGAGAAGAACTCAGTGAACTGAGTTCTCCACCTGCCAGAAAGGCAAATCCCTAGGCCTGGAGGGCTGAGGTCCTCA    7680

AAGCAGGGAAGCCTGTAGGGTGAGAGGGAAATGGTCAGAGCTTACCATAAACATAAGAGAGGATAAACCCTGTTGGTGAG    7760

AAGAGGAGGGAGCCAGGATCAAGACCAAGTCAACCTGGGTTATGGTTTAGTCTTTTTTTTTTTAGAGAAGCACAAAGAGGT    7840

TGCCATTGACCACCACTAACCAGTATCCCTGCTTTTCTCCCAATATCAGGCGAAGACTTATGAAGCAAGGCTCAGCAGTC    7920

CCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGGTCTTCCGCTCTTGCCCCATTGGTGAGAG    8000

CAAACCCCTCCTCAGTGGACAGCAGGTCTGAGTGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGT    8080

CTTTTCTCTGGTCTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG ←————————————SIL9    (SEQ ID NO: 14)    8138
```

Figure 2 (suite 2)

```
cDNA CH    GGTCTTTGGTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCC 60
cDNA RPE1  ------------------------------------------------------------


cDNA CH    ATGTGGCTCTGATGGGTGTTCTTCTGGCTGTAAGGACCACAGAAGGACCCAGAGACAGGG 120
cDNA RPE1  ------------------------------------------------------------


cDNA CH    ACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAG 180
cDNA RPE1  ------------------------------------------------------------


cDNA CH    AGTGGACAGAAAGCCAGGGGCCTGACTGCTGGAGAGGTGGCCACATATCCCTGAAGGTCA 240
cDNA RPE1  ------------------------------------------------------------


cDNA CH    GCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTCTATTGCCTTGCACTTTC 300
cDNA RPE1  ------------------------------------------------------------


cDNA CH    CTAAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCA 360
cDNA RPE1  ------------------------------------------------------------


cDNA CH    ATGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTGATGATACCTGCA 420
cDNA RPE1  ------------------------------------------------------------


cDNA CH    TCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTT 480
cDNA RPE1  ------------------------------------------------------------


cDNA CH    ATGTCTGGAAGACCTGGGACCAATACTGGCAAGTTCTGGGGGGCCCAGTGTCTGGACTGA 540
cDNA RPE1  ------------------CCAATACTGGCAAGTTCTGGGGGGCCCAGTGTCTGGACTGA 41
                             ********************************************

cDNA CH    GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC 600
cDNA RPE1  GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC 101
           ************************************************************

cDNA CH    GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG 660
cDNA RPE1  GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG 161
           ************************************************************

cDNA CH    ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC 720
cDNA RPE1  ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC 221
           ************************************************************

cDNA CH    GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT 780
cDNA RPE1  GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT 281
           ************************************************************

cDNA CH    TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT 840
cDNA RPE1  TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT 341
           ************************************************************

cDNA CH    CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG 900
cDNA RPE1  CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG 401
           ************************************************************

cDNA CH    TGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG 960
cDNA RPE1  TGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG 461
           ************************************************************
```

Figure 3

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cDNA CH    ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG 1020
cDNA RPE1  ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG 521
           ************************************************************


cDNA CH    AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCCTGGCACCACAGTTG 1080
cDNA RPE1  AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCCTGGCACCACAGTTG 581
           ************************************************************


cDNA CH    GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG 1140
cDNA RPE1  GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG 641
           ************************************************************


cDNA CH    TCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG 1200
cDNA RPE1  TCTTAAGTACCACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG 701
           ********** *************************************************


cDNA CH    TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGG 1260
cDNA RPE1  TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGG 761
           ************************************************************


cDNA CH    AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA 1320
cDNA RPE1  AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA 821
           ************************************************************


cDNA CH    TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG 1380
cDNA RPE1  TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG 881
           ************************************************************


cDNA CH    TCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC 1440
cDNA RPE1  TCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC 941
           ************************************************************


cDNA CH    TCACCCTGGACATTGTCCAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCA 1500
cDNA RPE1  TCACCCTGGACATTGTC---AGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCA 998
           *****************   ****************************************


cDNA CH     GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT 1560
cDNA RPE1   GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT 1058
            ***********************************************************


cDNA CH    GCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGC 1620
cDNA RPE1  GCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGC 1118
           ************************************************************


cDNA CH    CCCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT 1680
cDNA RPE1  CCCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT 1178
           *********************************************** ************


cDNA CH    ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG 1740
cDNA RPE1  ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG 1238
           ************************************************************


cDNA CH    TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG 1800
cDNA RPE1  TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG 1298
           ************************************************************


cDNA CH    TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT 1860
cDNA RPE1  TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT 1358
           ************************************************************


cDNA CH    CAGCAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG 1920
cDNA RPE1  CAGAAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG 1418
           *** ********************************************************
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Figure 3 (suite 1)

```
cDNA CH    TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1980
cDNA RPE1  TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1478
           ************************************************************


cDNA CH    TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 2040
cDNA RPE1  TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 1538
           ************************************************************

cDNA CH    CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 2086    (SEQ ID NO: 15)
cDNA RPE1  CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 1584    (SEQ ID NO: 16)
           **********************************************
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Figure 3 (suite 2)

```
Prot. CH    MDLVLRKYLLHVALMGVLLAVRTTEGPRDRDWLGVSRQLRIKAWNRQLYPEWTESQGPDC 60
Prot.RPE1   ------------------------------------------------------------


Prot.CH     WRGGHISLKVSNDGPTLIGANASFSIALHFPKSQKVLPDGQVIWANNTIINGSQVWGGQL 120
Prot.RPE1   ------------------------------------------------------------


Prot.CH     VYPQEPDDTCIFPDGEPCPSGPLSQKRCFVYVWKTWDQYWQVLGGPVSGLSIGTDKAMLG 180
Prot.RPE1   ----------------------------------QYWQVLGGPVSGLSIGTDKAMLG 23
                                              ***********************

Prot.CH     TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 240
Prot.RPE1   TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 83
            ************************************************************

Prot.CH     ALQLHDPSGYLAGADLSYTWDFGDSTGTLISRALTVTHTYLESGPVTAQVVLQAAIPLTS 300
Prot.RPE1   ALQLHDPSGYLAGADLSYTWDFGDSTGTLISRALTVTHTYLESGPVTAQVVLQAAIPLTS 143
            ************************************************************

Prot.CH     CGSSPVPGTTDRHVTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 360
Prot.RPE1   CGSSPVPGTTDRHVTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 203
            ************************************************************

Prot.CH     TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 420
Prot.RPE1   TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 263
            ************************************************************

Prot.CH     EPAGSNTSSFMPTEGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIVQGIE 480
Prot.RPE1   EPAGSNTSSFMPTEGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIV-SIE 322
            *******************************************************. **

Prot.CH     SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL 540
Prot.RPE1   SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL 382
            ************************************************************

Prot.CH     HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLLASL 600
Prot.RPE1   HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLLASL 442
            ************************************************************

Prot.CH     IYRRRLMKQGSAVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLSGQQV 649   (SEQ ID NO: 17)
Prot.RPE1   IYRRRLMKQGSEVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLSGQQV 491   (SEQ ID NO: 18)
            ********** *************************************
```

Figure 4